

OM of: US-09-805-550-2 to: EST: * out_format: pfs

Date: Aug 31, 2002 4:58 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-MODEL=frame+ .p2n.model -DEV=xih
-Q=/cgn2_1/USPTO.spool/US09805550/cunat_29082002.160721_29030/app-query.fasta.1.897
-DB=EST -OPMT=fastap -SUPFL=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -IOOPT=0.000 -IOGAPEXT=0.000 -IOGAPOP=4.500
-IOGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-IOGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELDP=6.000
-DELEX=7.000 -START=1 -MATRIX=blotsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEADSIZE=500
-MINLEN=6 -MAXLEN=200000000 -USER=US09805550.cgnl.1.3201
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NCPU -WAIT -THREADS=1
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Search information block:

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Query: US-09-805-550-2
Query Length: 405
Database: EST: *
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 2392.770000
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gb_est1:AM155658	955.00	1119.64	4.1e-53	589	1	AM155658 614097011.yl 614 - roc
gb_est1:AM057042	937.00	1098.77	5.9e-52	580	1	AM057042 66000808.xl 660 - Mix
gb_est1:AT881646	925.00	1083.29	4.3e-51	685	1	AT881646 606071012.yl 606 - Est
gb_est1:BE602523	895.00	1047.66	4.1e-49	735	1	BE602523 HVSMH009914f Hordeum
gb_est1:AT151316	884.00	1037.00	1.6e-48	575	1	AT151316 IPL_70.A12.bl.A003 fnc
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gb_est1:BI925179	837.00	979.67	2.5e-45	761	1	BI925179 EST545068 tomato flower
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gb_est1:BM078237	808.00	946.76	1.7e-43	685	1	BM078237 EST1116-H10.T3 ISDM-T
gb_est1:AM000280	803.00	942.63	2.9e-43	565	1	AM000280 614010804.yl 614 - roc
gb_est1:BG445328	781.50	914.35	1.1e-41	810	1	BG445328 GA_Ea0027122f Gossyp
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gb_est1:AV928200	774.00	906.28	3.1e-41	750	1	AV928200 AV928200 K. Sato unpub
gb_est1:BF586390	763.00	894.82	1.4e-40	642	1	BF586390 FMI_28.E12.g1.A003 fnc
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gb_est1:BG585286	757.00	885.68	4.4e-40	817	1	BG585286 EST487049 MHAM Medicago
gb_est1:BI305515	756.50	888.47	3.1e-40	559	1	BI305515 NL_0.E13 Drought stress
gb_est1:BM337351	753.00	882.39	6.7e-40	700	1	BM337351 EST149-E08.T3 ISDM5-R
gb_est1:AM331092	751.00	880.24	8.8e-40	685	1	AM331092 707047803.xl 707 - Mix
gb_est1:BE035647	746.50	871.93	2.5e-39	967	1	BE035647 MO13A05 MO Mesembryant
gb_est1:BG415925	739.00	865.54	3.8e-39	741	1	BG415925 HVSMH0009506f Hordeum
gb_est1:AM097027	734.50	860.62	1.1e-38	714	1	AM097027 AU097027 Rice shoot OR
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gb_est1:BG588991	725.00	848.52	5.1e-38	801	1	BG588991 EST490800 MHRP - Medica
gb_est1:BE704885	721.50	844.26	8.9e-38	817	1	BE704885 SC01.02C08.A SC01AARD
gb_est1:BF928270	721.00	846.90	6.3e-38	568	1	BF928270 WHE2165.H04.P0725 Triti
gb_est1:BM380735	716.00	839.60	1.6e-37	670	1	BM380735 MES524-C09.univ ISDM6
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gb_est1:BI947481	715.00	841.08	1.3e-37	897	1	BI947481 614047804.xl 614 - roc
gb_est1:BG445485	711.50	831.93	4.3e-37	880	1	BG445485 GA_Ea0028006f Gossyp
gb_est1:BE357293	707.50	830.55	5.1e-37	607	1	BE357293 DGL_148.C01.bl.A002 Dd
gb_est1:BE358080	702.50	826.51	8.6e-37	496	1	BE358080 DGL_24.C07.bl.A002 Dd
gb_est1:BM113219	695.50	815.40	3.6e-36	691	1	BM113219 EST560755 potato roots
gb_est1:BM266651	695.00	815.18	3.7e-36	663	1	BM266651 MES3184-H08.T3 ISDM5-R
gb_est1:BE357362	692.00	813.62	4.5e-36	533	1	BE357362 DGL_148.C01.g1.A002 Dd
gb_est1:AV922620	690.00	809.75	7.4e-36	634	1	AV922620 AV922620 K. Sato unpub
gb_est1:BE214515	687.00	805.14	1.3e-35	718	1	BE214515 HV_Ceb00032f Hordeum
gb_est1:BE917857	686.50	806.23	1.2e-35	595	1	BE917857 OVL_7.A02.bl.A002 Ovar

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gb_est1:BG344194 + 686.00 802.81 1.8e-35 819 1 BG344194 HVSMH0008A20f Hord
gb_est1:BI211965 + 682.50 801.77 2.1e-35 581 1 BI211965 IPL_62.F12.bl.A002
gb_est1:BE067283 + 681.50 799.94 2.6e-35 626 1 BE067283 st37908.yl Gm-cl1067
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seq_name: gb_est1:AM331091

seq_documentation_block:

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LOCUS AM331091 657 bp mRNA linear EST 31-JAN-2000
DEFINITION 707047803.xl 707 - Mixed adult tissues from Walbot lab (SK) Zea
ACCESSION AM331091
VERSION AM331091.1 GI:6827448
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 657)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707047 row: B column: 03.
Location/Qualifiers
1. 657
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10b"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
vector: pGAD10; Site: 1; EORI: cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1. 657
Location/Qualifiers

BASE COUNT 158 a 182 c 161 g 156 t
ORIGIN
alignment_scores:
Quality: 1012.00 Length: 218
Ratio: 4.842 Gaps: 0
Percent Similarity: 95.872 Percent Identity: 92.202

alignment_block:
US-09-805-550-2 x AM331091

Align seg 1/1 to: AM331091 from: 1 to: 657

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3 GCCACAGCTGAAGCGACCTCCAGTCACAGACTCGCTGCCAGC 52
GCCACAGCTGAAGCGACCTCCAGTCACAGACTCGCTGCCAGC 52
135 aAlaThValAlaAlaTrnAspAspAlaAspValTyrSerAlaAlaAla 152
|||||
53 TGCACAGCTGCTGATCGATGATGATGATGATGATGATGATGATGAT 102
TGCACAGCTGCTGATCGATGATGATGATGATGATGATGATGATGAT 102
152 eArslLeuValPhgGlyAsnAsnLeuGluGlnTrnTrnGlnGlnTrn 168
|||||
103 GCAACCTTGATGACGACCACTGACGACGACGACGACGACGACGAC 152
GCAACCTTGATGACGACCACTGACGACGACGACGACGACGACGAC 152

169 AspmctgLyGlyGlyThrTrpGluArgAspThrValValArgAlaLeuAr 185
 |||||
 153 GACATGGGGGTGGTACTGTGGAGCGGTGTACAGTGTCTGCTACG 202
 |||||
 155 GAlaAlaTyrAsnAsnProGluArgAlaAlaAspTyrLeuTyrSerGlyI 202
 |||||
 203 TGCTGCATATATATACCTGAGAGAGCTATAGACTACCTGATTTCTGGAA 252
 |||||
 202 LeProGluAsnValGluValGlnProValAlaArgAlaProAlaAlaGly 218
 |||||
 253 TTCCTGAGAAATGTGGAGGCTCCGCGTGGCCGAGCACCTCTGCTGGC 302
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 219 GInGInThrAsnGInGInAlaAlaSerProAlaGInProAlaValAlaLe 235
 |||||
 303 CAAACAACAAATCAGCAGGCTCCATCACCAAGCTCAGCCAGCAGCTGCACC 352
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 225 uProValGInProSerProAlaSerAlaGlyProAsnAlaAsnProLeuA 252
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 353 ACCAGTGCAGTATCTGCCGCTCTGCAGAGGCTTACGCAAAATCCTCTGA 402
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 252 snLeuPheProGInGlyValProSerGlyGlySerAsnProGlyValVal 268
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 403 ACCTTTTCCTCAGGAGTGTCCCAAGTGTGGGCCAATCCAGTGTGTGT 452
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 269 ProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGInLeuProGInPh 285
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 453 CCAGCTGCAGGATCTGTGCTCCCTTGTGCTGCAGCAGCTTCCACAGTT 502
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 285 eGInAlaLeuLeuGInLeuValGInAlaAsnProGInIleLeuGInProm 302
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 503 TCACACACAGCTTTCAGTGTGTCCAGGCTATCTCAAAATCTTGACGCCAA 552
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 302 eLeuGInGInLeuGlyGlySerGInAsnProGInIleLeuArgLeuIleGIn 318
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 553 TCCTTCACAGAACTAGGCAAAACCAACCAATCCTCGTTGATTCAG 602
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 319 GluAsnGInAlaGlnPheLeuArgLeuValAsnGInUserProGInGlyI 335
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 603 GAAATTCAGAGTGAAGTGTCTGCTGCTGTGAAACGAAATCCGAGAGGTGG 652
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 335 YPro 336
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 653 TCCT 656

seq_name: gb_ests:AW155658
 seq_documentation_block: 589 bp mRNA linear EST 04-NOV-1999
 LOCUS AW155658
 DEFINITION 614097D1.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
 mRNA sequence.
 ACCESSION AW155658
 VERSION AW155658.1 GI:6227129
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 589)
 Walbot V
 Zea ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 614097 row: D column: 11.
 Location/Qualifiers

SOURCE 1. 589
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="614 - root cDNA library from Walbot Lab"
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 /lab_host="X10LR"
 /note="Organ: root; Vector: plusescriptII SK+; Site:1;
 Ecotri; Site_2: XhoI; 3-4 days old root tissue from Walbot
 Lab (LM)"
 BASE COUNT 139 a 169 c 139 g 140 t 2 others
 ORIGIN

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 Ratio: 4.974 Caps: 0
 Percent Similarity: 98.969 Percent Identity: 96.907

alignment_block:
 US-09-805-550-2 x AW155658 ..

Align seg 1/1 to: AW155658 from: 1 to: 589

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 6 AGTCATCAGTTGCAAGAACACCAACACAGGCTCCTGTTGCCACAGCTGA 55
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 122 uThrAlaProProSerValGInProGInAlaAlaProAlaAlaThrValA 139
 |||||
 56 AACGCACCTCCAAAGTCCCAACCTCAGGCTCTCCAGTGTGACGGTTG 105
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 139 lAlaAlaThrAspAspAlaAspValTyrSerGInAlaAlaSerAsnLeuVal 155
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 106 CTGCTACTATGATGTGTGATGTGTACAGTACAGCAGCTTCAAACTTGA 155
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 156 PheGlyAsnAsnLeuGInGInThrIleGInIleLeuAspMetGlyI 172
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 172 yGlyThrTrpGluArgAspThrValValArgAlaLeuArgAlaAlaTyrA 189
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 189 snAsnProGluArgAlaAlaAspTyrLeuTyrSerGlyIleProGluAsn 205
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 206 ValGluAlaGlnProValAlaArgAlaProAlaAlaGlyGInGInThrAs 222
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 306 GTGGAGGCTCAGCCTGTGCTCCGAGACACTGCTGTGGCCAAACAAACA 355
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 222 nGInGInAlaAlaSerProAlaGlnProAlaValAlaLeuProValGInP 239
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 356 TCAGCAGGCCGATCACCCGCTCAGCCAGCACTGTGATTCAGAGTGCACC 405
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 239 roSerProAlaSerAlaGlyProAsnAlaAsnProLeuAsnLeuPhePro 255
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 406 CATCACCTGCTCTGAGGGCTTAATGCAAAATCTTGAACCTTTTCT 455
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 256 GInGlyValProSerGlyGlySerAsnProGlyValValProGlyAlaG 272
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 456 CAGGCTGTCCAAAGGGGNGGTCCAAACCAAGCGTTATTCAGAGTGTGG 505
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 272 ySerGlyAlaLeuAspAlaLeuArgGInLeuProGInPheGInAlaLeuL 289
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 506 ATCTGGNGCCTTGATGCTTGCAGACGCTTCACAGTTTCAAGACATCC 555
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 289 eGInLeuValGInAlaAsnProGInIleLeu 299
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 556 TTCAGTTAGTCCAGGCTATCTCAAAATCTTG 587

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seq_documentation_block:
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DEFINITION 660008A08.y1.660 - Mixed stages of anther and pollen Zea mays cDNA,
            mRNA sequence.
ACCESSION  AW057042
VERSION    AW057042.1   GI:5932681
KEYWORDS   EST.
SOURCE      Zea mays.
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ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            Clade; Panicoidae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 580)
AUTHORS   Walbot,V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
JOURNAL   Unpublished (1999)
COMMENT   Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 660008 row: A column: 08.
            Location/Qualifiers
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                                Directionally sequenced with 5' end at the EcoRI site.
                                Created by Amie Franklin."
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118 ValAlaThrAlaGluThrAlaProSerValGlnProGlnAlaAlaPr 134
114 GTTGCACACACTGAAACGGCACCTCCACAGTCCACCTCAGCTGCTCC 63
134 oAlaAlaThrValAlaAlaThrAspAlaAspValTyrSerGlnAla 151
64 AGCTGCTACGGTGTGCTGCTACTGATGATGCTGATGCTACAGTCAGCAG 113
151 laSerAsnLeuValIphcGlyAsnAsnLeuGlnGlnThrIleGlnGlnIle 167
114 CTTCACAACCTTGTATCTGGCACACATCTAGACAGACTATCCAACAATT 163
168 LeuAspMetCysGlyGlyThrTTPGluArgAspThrValValArgAlaLe 184
164 CTTCAGACATGGTGTGTGTACATGGAACCTGATACCTGTCGTGCTCT 213
184 uATGAlaAlaATyrAsnAsnProGluArgAlaIleAspTyrLeuTyrSerG 201
214 ACGTGCTGCATACATACACCCGAGAGAGCTATAGACTTACTGATTTCTG 263

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201 lTyleProGluAsnValGluAlaGlnProValAlaArgAlaProAlaAla 217
264 GAATTCCTGAGAAATGTGAGAGCTCAGCTGTGCTCCGAGCAGCAGCTGCT 313
218 GlyGlnGlnThrAsnGlnGlnAlaAlaSerProAlaGlnProAlaValAl 234
314 GGCCACCAACCAAAATCAGCAGCGGCATCCAGCCGCTCAGCAGCAGTTGC 363
234 aLeuProValGlnProSerProAlaSerAlaGlyProAsnAlaAsnProL 251
364 ATTCGCCAGTGCAGCAGCAGCTGCTGCTGCGAGGCCCTAATGCAATCTT 413
251 euAsnLeuPheProGlnGlyValProSerGlyGlySerAsnProGlyVal 267
414 TGAACCTTTTCCACAGGTTCCAGAGTGTGGGTCACACCCAGGTGTT 463
268 ValProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnLeuProG 284
464 GTTCACAGTGCAGAGATCTGTGCTCTTGATGCTTGGACAGCTTCACCA 513
284 nPhcGlnAlaLeuGlnLeuValGlnAlaAsnProGlnIleLeuGlnP 301
514 GTTCAAGCACTCCTTCATGTTAGTCCAGGCTATCTCAATCTTGACAGC 563
301 roMetLeuGln 304
564 CAATGCTTAG 574
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seq_documentation_block:
LOCUS      AI881646                685 bp    mRNA    linear    EST 02-FEB-2000
DEFINITION 606071D12.y1.606 - Ear tissue cDNA library from Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION  AI881646
VERSION    AI881646.1   GI:5566780
KEYWORDS   EST.
SOURCE      Zea mays.
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            Clade; Panicoidae; Andropogoneae; Zea.
            1 (bases 1 to 685)
REFERENCE  1
AUTHORS   Walbot,V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
JOURNAL   Unpublished (1999)
COMMENT   Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 606071 row: D column: 12.
            Location/Qualifiers
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                                /organism="Zea mays"
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                                lab"
                                /tissue_type="mixed"
                                /dev_stage="ear length from 0.5 cm - 2.0 cm"
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                                lab"
BASE COUNT 184 a      187 c      174 g      140 t
ORIGIN

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Quality: 925.00 Length: 191
Ratio: 4.894 Gaps: 0
Percent Similarity: 98.953 Percent Identity: 98.953

alignment_block:

US-09-805-550-2 x AI881646 ..

Align seg 1/1 to: AI881646 from: 1 to: 685

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1 MetLysLeuAsnValLysThrLeuYsglyThrAsnPhgUllleGluAl 17
110 ATGAAGCTTAACGTCAGACCCCTCAAGGGCACCACCTTGACATGAGGC 159
17 aserProaspAlaSerValAlaAspValLysArgilleGlyThrThg 34
150 GAGCCCCCGATGCGTTCGATGTGAAGAGATCATATGAGACACATC 209
34 lnglGlnSerThrTyrrArgAlaAspGlnGlnMetLeuIleTyrglngly 50
210 AAGGTCAGAGTACTACCGGGCGGACGACCAATGCTCATATACCAAGGG 259
51 LysIleLeuLysAspGluThrThrLeuGlnSerAsnGlyValAlaGluAs 67
260 AAAATTCGAAGAGTGAACCACTTGGAAGCAACGAGGTGCTGAGAGA 309
67 nSerPheLeuValIleMetLeuSerLysAlaLysAlaSerSerSergIya 84
310 CAGCTTCCCTGTTATATGTTGTCCAGGCTTAAGGCATCATCGATGCGAG 359
84 laSerThrAlaThrThrAlaLysAlaProAlaThrLeuAlaGlnProAla 100
360 CTTCTACCGCTACTACTGCAAAAGCTCCTGCAACTGTGGCCCAACCTGCT 409
101 AlaProValAlaProAlaAlaSerValAlaArgThrProThrGlnAlaPr 117
410 GCCCGTGGGCCCCGTGCGCATCAGTTGCAAGACACACAGACAGGCTCC 459
117 oValAlaThrAlaGluThrAlaProProSerValGlnProGlnAlaAlaPr 134
460 TGTGCCACAGCTGAACGGCGACCTCCAAAGTGTCCACCTCAGGCTGCTCC 509
134 roAlaAlaThrValAlaAlaThrAspAlaAspAlaTyrSergInAla 150
510 CAGCTGCTACGGTTCCTGCTACTGATGATGCTGATGTGACAGTCAAGCA 559
151 AlaSerAsnLeuValPheGlyAsnAsnLeuGlnGlnThrIleGlnGlnI 167
560 GCTCAAAACCTGTATCTGGCAACAATCTAGAACAGACATCAACAAT 609
167 eLeuAspMetGlyGlyGlyThrTTPGluArgAspThrValAlaArgAlaL 184
610 TCTTACACATGGGTGCTGCTACATGGAACGTGATCTGCTGCTGCTC 659
184 euArgAlaAlaTyrAsnAsnPro 191
660 TACGTGCTGCTACATACCAACCG 682

seq_name: gb_est2:BE602523
seq_documentation_block:
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DEFINITION HVSMEH009J14f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH009J14f,
mRNA sequence.
ACCESSION BE602523
VERSION BE602523 GI:13190364
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.

```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 735)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu,
'Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Aug 21, 2000 this sequence version replaced gi:9860084.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total hg bases = 500
Seq primer: AATTAACCTTCACATTAAGG
High quality sequence start: 12
High quality sequence stop: 609.
Location/Qualifiers
1. 735
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH009J14f"
/clone_id="Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SD Close, T.J. Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give plasmid SK(-) cDNA phageids
(Choi) in the T.J. Close lab at the University of California,
Riverside. Phageids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close T.J., Wing R., Kleinhofs A., Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gppages/bgn/31/cover.html)"

BASE COUNT 179 a 166 c 199 g 171 t
ORIGIN

alignment_scores:

Quality: 895.00 Length: 219
Ratio: 4.520 Gaps: 2
Percent Similarity: 90.411 Percent Identity: 82.648

alignment_block:

US-09-805-550-2 x BE602523 ..

Align seg 1/1 to: BE602523 from: 1 to: 735

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188 TTTAAAsnProGluArgAlaAlaAspTyrLeuTyrSergIleProG 204
|||||
10 TTTACCAACCTGAGAGGCGTATGCTACGCTGCTGGAATACCTGGA 59
204 uAsnValGluAlaGlnProValAlaArgAlaProAlaAlaGlyGlnG 221

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60 ATCCGAGAGAGGCCCCACCTGTGGCTGAGCAGCTGCTCTCAACAGG 109
221 hr...AnsgInGlnAlaIaSerProAlaGlnProAlaValAlaLeuPro 236
110 CAAAAACCGCAGGAGCTCATCTCAGGCTCAGGCTGACCTACCGGCA 159
237 ValGlnProSer...ProAlaSerAlaGlyProAsnAlaAsnProLeuAs 252
160 GTGCACCCATCTGTGTGTCCTCTGCTGGCCCTAAATCCGAATCCTCTAAA 209
252 nleuPheProGlnGlyValProSerGlySerAsnProGlyValValP 269
210 CCTTTCCACAGAGGTGTTCAGAGTGGGGCCAAATGCTGTGCTGTG 259
269 roGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnLeuProGlnPhe 285
260 TGGGTGCGGCTGCGGCTGATGATGATGATGATGATGATGATGATGATG 309
286 GlnAlaLeuLeuGlnLeuValGlnAlaAsnProGlnLeuGlnProme 302
310 CAAGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 359
302 tleuGlnGlnLeuGlyGlyGlnAsnProGlnLeuArgGlnLeuGln 319
360 GCTTCAGAGAGCTGGGAAACAAATCCACAGATCTGCGGTGATTCAGG 409
319 luanGlnAlaGlnPheLeuArgLeuValAsnGlnSerProGlnGlyGly 335
410 AAATACAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 459
336 ProGlyGlyAsnLeuGlnGlyGlnLeuAlaAlaValProGlnThrLe 352
460 GCTGCGGGAATATATAGGCGCATGCTCAATGCCACAGGCGAT 509
352 utrValThrProGlnGlnArgGlnAlaLeuGlnArgLeuGlnGlyMetG 369
510 TCAAGTACTCCAGAAAGACGAGGAGCCATCCAGGCTTGAGCAATGG 559
369 lypPheAsnArgGlnLeuValLeuGlnValPhePheAlaCysAsnLysAsp 385
560 GGTTCATGCTGAGCTGTGTGTGAGAGCTCTTTCATGATGACAAAGGAT 609
386 GlnGlnLeuThrAlaAsnTyrLeuLeuAspHisGlyHisGlnPheAsp 402
610 GAAGAAGCTGCTGCAACATATCTTTGGATCATGCGCAGAGTTGAGGA 659
402 pGlnGln 404
660 ACAACAA 666
seq_name: gb_est2:BI351316
seq_documentation_block:
LOCUS BI351316 575 bp mRNA linear EST 31-Jul-2001
DEFINITION IPI_70_A12.b1_A002 Immature pannicle 1 (IPI) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BI351316
VERSION BI351316.1 GI:15045758
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 575)
AUTHORS Klein,R.R., Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M. and Pratt
,L.H.
TITLE An EST database from Sorghum: developing preanthesis pannicles
JOURNAL Unpublished (2001)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia

```

```

Plant Sciences Building, Km. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpatr@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three prime sequences, which are obtained with PolyTmix or T7
sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 457
POLYA-No.

FEATURES
    source          Location/Qualifiers
1..575
    /organism="Sorghum bicolor"
    /cultivar="BTx623"
    /db_xref="taxon:4558"
    /clone_lib="Immature pannicle 1 (IPI)"
    /note="Organ: Developing preanthesis pannicles; Vector:
    Bluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
    Site_2: EcoRI; The library was made from poly-A RNA in the
    cloning vector lambda Zap II. Clones to be sequenced were
    prepared by mass excision."
BASE COUNT      137 a      147 c      155 g      136 t
ORIGIN
alignment_scores:
    Quality: 884.00      Length: 182
    Ratio: 4.966      Gaps: 0
    Percent Similarity: 97.802      Percent Identity: 94.505
alignment_block:
US-09-805-550-2 x BI351316 ..
Align seg 1/1 to: BI351316 from: 1 to: 575
224 GlnAlaIaSerProAlaGlnProAlaValAlaLeuProValGlnProse 240
6 AGGCGCTCCATCGCCTGCTCAGCCAGCAGTTCACCTCCAGTCGACGATC 55
240 rProAlaSerAlaGlyProAsnAlaAsnProLeuAsnLeuPheProGln 257
56 CGTGCCTCTGCGAGGCGCTATGCAAAATCCTCTAACCTTTCTCAGG 105
257 lylValProSerGlyGlySerAsnProGlyValValProGlyAlaGlySer 273
106 GTGTTCCAGTGGTGGGCGCAATCAGGTGTGTTCACAGTGCAGATCT 155
274 GlyAlaLeuAspAlaLeuArgGlnLeuProGlnPheGlnAlaLeuGln 290
156 GTGCGCTTGATGCTTCGCGACAGCTTCACAGTTCACAGCAGCTGTCA 205
290 nleuValGlnAlaAsnProGlnLeuGlnProMetLeuGlnLeuGln 307
206 GTTGTGTCAGGCTATATCTCAATCTTACAGCCATGCTTCAAGATAG 255
307 lylGlnAsnProGlnLeuArgLeuLeuGlnGlnGlnGlnGlnGlnGln 323
256 GCAAAACAAACCCCAAAATCTGCGGTGATTCAGAAATCAACGCTGAG 305
324 PheLeuArgLeuValAsnGlnSerProGlnGlyGlyProGlyGlyAsn 340
306 TTCTCCGCTGCTGGTAATGAAATCCCTGAGGAGGTGCTGAGGAAACAT 355
340 eleuGlyGlnLeuValAlaValAlaValProGlnThrLeuThrValThrProG 357
356 ACTGAGTCACTGAGCTGATGCTCAACAGCTGACGGTTACACAG 405
357 lueGlnArgGlnAlaIleGlnArgLeuGlnGlyMetGlyPheAsnArgGln 373
406 AGGAACGGAGGCAATCCAGCGCTTGAGGGGAGATGGGTTCAACCGTAG 455
374 leuValLeuGlnValPhePheAlaCysAsnLysAspGlnLeuThrAla 390

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|||||
456 CATGCGTAGAAGTTTCTTTCATGACCAACGAGGAGACCTTGCGCC 505
|||||
390 aasntyrleuLeuaspHisGlyHisGluPheaspArgInglIn 405
|||||
506 CAACCTACCTTGTGATCATGGCCATGAGTTTGACGACGACGACAA 551
|||||
seq_name: gb_est2:BF586471

seq_documentation_block:
LOCUS BF586471 597 bp mRNA linear EST 12-DEC-2000
DEFINITION Fm1.28_E12.D1.A003 floral-induced meristem 1 (Fm1) Sorghum
PROPIONQUUM cDNA, mRNA sequence.
ACCESSION BF586471
VERSION BF586471.1 GI:11678795
KEYWORDS EST.
SOURCE Sorghum propinquum.
ORGANISM Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 597)
Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and Pratt
/L.H.
An EST database from Sorghum: floral-induced meristems
unpublished (2000)
JOURNAL Contact: Cordonnier-Pratt MM
COMMENT Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: empratleuga.edu
Sequences have been trimmed to exclude Polya, vector and regions
below phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 534
POLYA-No.

FEATURES
Source
1..597
/organism="Sorghum propinquum"
/db_xref="taxon:132711"
/clone_lib="floral-induced meristem 1 (Fm1)"
/note="Organ: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
EcoRI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda Zap II. Clones to be sequenced were prepared by
mass excision."

BASE COUNT 154 a 161 c 151 g 131 t
ORIGIN

alignment_scores:
Quality: 870.50 Length: 194
Ratio: 4.655 Gaps: 1
Percent Similarity: 96.392 Percent Identity: 92.784

alignment_block:
US-09-805-550-2 x BF586471 ..
Align seg 1/1 to: BF586471 from: 1 to: 597

1 MetLysLeuAsnValLysThrLeuLysGlyThrAsnPheGluIleGluAl 17
|||||
14 ATGAAGCTTAACGTCACGACCCCTCAAGGACCAACTTCGAGATCGAGGC 63
|||||
17 aSerProAspAlaSerValAlaAspValLysArgIleIleGluThrTrpG 34

```

```

|||||
64 GAGCCCGGATGCGTCGTGCTGAGGTGAAGAGATCATGAGACCCTC 113
|||||
34 lnglYglInserThrTyrArgAlaAspGlnGlnMetLeuIleTyrGln 50
|||||
114 AGGCTCAGAGTACCTACACCGCGACACACCAATATCTCTATACCAAGG 163
|||||
51 LysIleLeuLysAspGluThrThrLeuGlnSerAsnGlyValAlaGluAs 67
|||||
164 AAAATCTTCAGAGATGAGACCACTTGGAAAGCAACGAGAGTTGCTGAGA 213
|||||
67 nSerPheLeuValIleMetLeuSerLysAlaLysAlaSerSerGlyA 84
|||||
214 CAGCTTCCTGTTATATATGTTCTCCAGGCTAAGGATGATGCTGAGTGAG 263
|||||
84 lAserThrAlaThrThrAlaLysAlaProAlaThrLeuAlaGlnProAla 100
|||||
264 CTTTACTGCTACTGCTGCAAAAGCTCCGCAACCTCGGCCCAACTGCT 313
|||||
101 .....AlaProValAlaProAlaAlaSerValAlaArgThrProTh 114
|||||
314 GCACCTGTAGCCCTGTGGCCCTGCTCATCATGTTGCAAGAACACTAC 363
|||||
114 nGlnAlaProValAlaThrAlaGluThrAlaProSerValGlnProG 131
|||||
364 ACAAGCTCCTGTTGCCACAGCTGAACGACACCTCCAGTGCACGACCTC 413
|||||
131 lAlaAlaProAlaAlaThrValAlaAlaThrAspAlaAspValTyr 147
|||||
414 AGCGTCTCTCTGCTCTACGAGTTGCTGCATCTGCGATGATGCTATGTCAC 463
|||||
148 SerGlnAlaAlaSerAsnLeuValPheGlyAsnAsnLeuGlnThrTl 164
|||||
464 AGTCAGGACGCTTCAACCTGTATCTGGCAACAATAGAACACACTAT 513
|||||
164 eGlnGlnIleLeuAspMetGlyGlyGlyThrTrpGluArgAspTrpVal 181
|||||
514 CCACCAAAATCTTGAACATGGGTGGTGTGACTGGACAGCTGATACAGTGG 563
|||||
181 aAlaArgAlaLeuArgAlaAlaLysAsnAspPro 191
|||||
564 TCCGTCCTGCTACGCTGCTGATATATTAACCT 595
|||||

seq_name: gb_est2:BI925179

seq_documentation_block:
LOCUS BI925179 761 bp mRNA linear EST 18-OCT-2001
DEFINITION EST545068 tomato flower, buds 0-3 mm lycopersicon esculentum cDNA
clone CP0A25B24 5' end, mRNA sequence.
ACCESSION BI925179
VERSION BI925179.1 GI:16230294
KEYWORDS EST.
SOURCE Lycopersicon.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eunasterids I; Solanales; Solanales; Solanales; Solanum;
Lycopersicon.
1 (bases 1 to 761)
van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,
Uterback,T., Van Aken,S., Romning,C.M., Nierman,M., Fraser,C.M.,
Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato flower tissue, 0-3 mm buds (2001)
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers

```



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23 ValAlaaspValLysArgIleIleGluThrGlnGlyGlnSerThrTy 39
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1 GTGGCGATGTAAAAAGACATAGAACTGTTCAAGGACGATGATTTA 50
39 rArgAlaaspGlnMetLeuIleTyrGlnGlyLysIleLeuLysaspG 56
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
51 TCGTCTTCAACAACAAATGCTAATCTAAGGAAAGTTCTTAAAGATG 100
56 LurThrLeuGluSerasnGlyValAlaGluasnSerPheLeuValIle 72
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
101 ACAGACAGCTGGCTGAAGACAGTGTCACTGAATAAGCTTATTTGATC 150
73 MetLeuSerLysAlaLysAlaSerSer.....SerGlyAlaSerTh 86
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
151 ATGTTAAACAAGAAATAGGTACAACTGGTACGCGTCAACGCTTCAAC 200
86 rAlaThrThrAlaLysAlaProAlaThrLeuAlaGlnProAlaProV 103
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
201 AGCTCTTCAACAAGAAAGCTCGAGGCAAGTAACTGCCAACAGCTCCA. 249
103 aAlaProAlaLaserValAlaArgThrProThrGlnAlaProValAla 119
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
250 ..GCACCAAGCTTCTACT.....GCACCTGTGCA 276
120 ThrAlaGluThrAlaProProSerValGlnProGlnAlaAlaProAla 136
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
277 ACGTCAGCTATGCGT.....GCACCTGCCACTGAATCTGCTCCTGTGC 320
136 aThrValAlaLaserValAlaLysAlaLysAlaLysAlaLysAla 153
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
321 TTCAGATCTCTCTTGTCAATCTGATGATTTATGCGCAAGCAGCATCTA 370
153 snLeuValPheGlyAsnAsnLeuGlnGlnThrIleGlnGlnIleLeuasp 169
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
371 ACGGTGTGACGGGAGTAAGTAGGAGGACATCCAAACAGATTCTTGAT 420
170 MetGlyGlyGlyThrTTPGluArgAspThrValValAlaGlnAlaLeu 186
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
421 ATGGGTGAGGAGGACTGCGACAGGACACTGTGTCCACGCCCTTCGTGC 470
186 aAlaTyrAsnAsnProGluArgAlaIleAspTyrLeuTyrSerGlyIleP 203
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
471 TCGTTATATATACCCAGAGAGAGCTGTGAATATTGTATCTGCGCATCC 520
203 rGluAsnValGluAlaGlnProValAlaArgAlaProAlaLaglyGln 219
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
521 CCGAGCAAGCTGAAGCTCCACCTGTGGCCGCTCTGTAGTTGGCAA 570
220 GlnThrAsnGlnAlaAlaLaserProAlaGlnProAlaValAlaLeuPr 236
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
571 ACCACAAAC...TCGTGCAACAACCTCAACAGCTGCACAAACGCGCAGC 617
236 oValGlnProSerProAlaLaserAlaGlyProAsnAlaAsnProLeuAsn 253
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
618 TATTT.....CCTGCAAGT...GGACCAATGCAAAATGCATTAGACC 655
253 eupheProGlnGlyValProSerGlyLysSerAsnProGlyValValPro 269
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
656 TCTTTCCCGAGGCGCTCCCAACATGGGTGCAAGT..... 690
270 GlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnLeuProGlnPheG 286
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
691 GGTCTGAGGCTGGCAGCTTGATTTTACGAACACTACACAGTTTCA 740
286 nAlaLeuGlnLeuValGlnAlaAsnProGlnIleLeuGlnPrometL 303
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
741 AGCTTTGGACCAATGCTGAAGCCAAATCCAAATATTGGAGGCCATGCG 790
303 eugInGluLeuGlyLysGlnAsnProGlnIleLeu..ArgLeuIleGln 319
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
791 TTCAAGAGGTGGGGAACAATAATCTATTATGAAAACTTATACAGAA 840

```

```

319 uAsnGlnAlaGluPheLeuArgLeuValAsnGluSerProGluGlyP 336
: ||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
841 GCCTCAGGCTGATTTCTTCTTGATCAAGCAAGCTGCGTGAAGTGGGA 890
336 rGly 337
|||
891 AGGGA 895

seq_name: gb_est1:AW399956

seq_documentation_block:
LOCUS AW399956 623 bp mRNA linear EST 07-FEB-2000
DEFINITION 707055C08.x1 707 - Mixed adult tissues from Walbot lab (SK) Zea
ACCESSION mays cDNA, mRNA sequence.
VERSION AW399956
KEYWORDS AW399956.1 GI:6918426
SOURCE EST.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 623)
REFERENCE Walbot V
AUTHORS Walbot V
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707055 row: C column: 08.

FEATURES
source
location/qualifiers
1..623
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"
"/issue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH108"
/note="Organ: tassel, kernel, silk, husk, root, leaf;
Vector: pGAD10; Site: 1; EcoRI: cDNA library from fully
differentiated maize tissues from an active Mutator
plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,
husk, root, leaf). Unidirectionally cloned."
BASE COUNT 158 a 175 c 167 g 122 t 1 others
ORIGIN

alignment_scores:
Quality: 812.00 Length: 174
Ratio: 4.749 Gaps: 0
Percent Similarity: 98.276 Percent Identity: 95.977

alignment_block:
US-09-805-550-2 x AW399956 ..

Align seg 1/1 to: AW399956 from: 1 to: 623

1 MetLysLeuAsnValLysThrLeuLysGlyTrrAsnPhgIleGluAl 17
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
102 ATGAAGCTTAACGTCAAGACCTCAAGGCGACCACTTGAGATGAGGCG 151
17 aserProAspAlaSerValAlaAspValLysArgIleIleGluThrThg 34
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
152 GAGCCCGCATGCGTGTGCTGAGAGTGAAGAGATTCATGAGACACATC 201
34 lngIleGlnSerThrTyrArgAlaaspGlnGlnMetLeuIleTyrGln 50

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|||||
202 AGGCTAGACTACCTACCGGGGAGCAGCAAAATGCTATATACCAAGG 251
51 Lys11leuLysAspGluThrThrLeuGlnSerAsnGlyAlaGlnAs 67
252 AAAATCTCAAGATGAGACCACTTGGAAAGCAGCAGACTGCTGAGA 301
67 nSerPheLeuValIleMetLeuSerLysAlaLysAlaSerSerGly 84
302 CACCTTCCTGTTATATATGTTGCACAGGCTTAAGGCATCTCGAGTG 351
84 LaserThrAlaThrThrAlaLysAlaProAlaThrLeuAlaGlnPro 100
352 CTCTACCACTACTGCTGCAAAAGCTCTGCACTGCGCCCAACCTGCT 401
101 AlProValAlaProAlaAlaSerValAlaArgThrProThrGlnAla 117
402 GCCCTGTGCCCCCTGCTGCATCAGTTGCAGAAACCAACACAGGCTCC 451
117 OValAlaThrAlaGluThrAlaProProSerValGlnProGlnAla 134
452 TGTGGCCACAGCTGAAGACGACCTCCAGTCCCAACCTCAGGCTGCTC 501
134 roAlaAlaThrValAlaAlaThrAspAlaAspValTyrSerGlnAla 150
502 CACCTGCTACGGTGTGCTACTGATGATGCTGATGTGTACAGCAGCA 551
151 AlSerAsnLeuValPheGlyAsnAsnLeuGlnGlnThrIleGlnGln 167
552 GCTTCAAACTTGTATCTGGCAGACAGCTAGAACAGCTATCCAAACA 601
167 eLeuAspMetGlyGlyGlyThr 174
602 TCTTGACATGGGTGTGTGTACA 623

seq_name: gb_est2:BM078237

seq_documentation_block:
LOCUS BM078237 685 bp mRNA linear EST 14-NOV-2001
DEFINITION MEST116-H10.T3 ISUM4-TN Zea mays cDNA clone MEST116-H10 3', mRNA
sequence.
ACCESSION BM078237
VERSION BM078237.1 GI:16925169
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 685)
Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
CTA TAG)

```

```

BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
FEATURES
source
1..685
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST116-H10"
/clone_1b="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/note="Vector: pT733PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5',
AAGTCGAGAAATTCGCGCGGCGGAGGAATTTTCTTTTCTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA polI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT733PAC vector. The library
then went through one round of normalization to COT value
of 5 based on the methods of Marcelo Bento Soares (genome
Research 6: 791-806, 1996)."
BASE COUNT 177 a 169 c 155 g 184 t
ORIGIN

alignment_scores:
quality: 808.00 Length: 158
Ratio: 5.114 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.367

alignment_block:
US-09-805-550-2 x BM078237/rev ..

Align seg 1/1 to reverse of: BM078237 from: 1 to: 685

248 AAlAsnProLeuAsnLeuPheProGlnGlyValProSerGlyGlySerAs 264
|||||
684 GCANAATCTTGAACCTTTTCTCAGGGGTCTCCAGAGTGAGGATCCAA 635
264 nProGlyValValProGlyAlaGlySerGlyAlaLeuAspAlaLeuArg 281
|||||
634 CCCAGGTGTTGTTCCAGGTGAGGATGCGTGCCTTTCATCTCCCTGGC 585
281 LLeuProGlnPheGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGln 297
|||||
584 AGCTTCCACAGTTTCAAGCACTCTTCAGTTAAGTCCAGGCTAAATCCCA 535
298 LLeuGlnProMetLeuGlnGlnLeuGlnGlyGlnAsnProGlnIleLe 314
|||||
534 ATCTTGACGCCAATGCTTCAAGAGCTAGTAAACAAACCCCAAAATCT 485
314 nArgLeuIleGlnGlnLysAsnGlnAlaGluPheLeuArgLeuValAsnGln 331
|||||
484 GCGGTGATTAGGAAATCAAGCTGACTTCTCCGCTGGTGAATGAT 435
331 eProGlnGlyGlyProGlyGlyAsnIleLeuGlnGlnLeuAlaAla 347
|||||
434 CTCTGAGGCTGTCCTGAGGAGAAATCAATGAGTCACTGCGAGCTGCT 385
348 ValProGlnThrLeuThrValThrProGlnLysArgGlnValAlaGln 364
|||||
384 GTGCCCAACAGCTGACAGTACCCAGAGGAGGAGGCTATCCACG 335
364 gLeuGlnGlyMetGlyPheAsnArgGluLeuValLeuGlnValPhePhe 381
|||||
334 GCTGAGGGAATGGGTTCAACCGTACCTTGTGTAAATTTTCTTTG 285
381 lAcYAsnLysAspGlnGluLeuThrAlaAsnTyrLeuLeuAspHisGly 397

```

```

|||||
284 CATGAAACAGACGACGAGCTTACAGCCACTCCTCGATCATGGC 235
398 Hhslupheaspapglnglncin 405
|||||
234 CATGAGTTTGACGACGACGACCA 211

seq_name: gb_est1:AM000280

seq_documentation_block:
LOCUS AM000280 565 bp mRNA linear EST 08-SEP-1999
DEFINITION 614010B04.y1 614 - root cDNA library from Walbot Lab zea mays cDNA,
mRNA sequence.
ACCESSION AM000280
VERSION AM000280.1 GI:5847201
KEYWORDS EST.
SOURCE zea mays.
ORGANISM zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 565)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614010 row: B column: 04.
FEATURES
location/Qualifiers
source 1..565
/organism="Zea mays"
/cultivar="W3"
/db_xref="taxon:4577"
/clone_id="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
/note="Organ: root; Vector: pBluescriptII SK+, Site_1:
EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"
BASE COUNT 139 a 133 c 148 g 145 t
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align_scores:
Quality: 803.00 Length: 157
Ratio: 5.115 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.726
alignment_block:
US-09-805-550-2 x AM000280 ..
Align seg 1/1 to: AM000280 from: 1 to: 565
249 AsnProLeuAsnLeuPheProGlnGlyValProSerGlyGlySerAsnPr 265
|||||
1 AATCTTTGAAACCTTTTCTCAGGGTGTTCCAAAGTGGTGCCAAACCC 50
265 cblYvalValProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnL 282
|||||
51 AGCGCTTAATCCAGGTCGCGATCGTGCCCTTGATGCTTGCCACACG 100
282 euProGlnPheGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGlnInle 298
|||||
101 TTCACAGATTCAAGCACCTCTTCAGTTAGTCACAGGCTTAATCCTCAATC 150
299 LeuGlnProMetLeuGlnGlnLeuGlnGlyGlnAsnProGlnInleLeuAr 315

```

```

|||||
151 TTGACGCCAATGCTTCAAGAGCTAGGTTAAACAACCCCAAAATCTCGCG 200
315 greulieglnGluAsnGlnAlaGluPheLeuArgLeuValAsnGluSerP 332
|||||
201 GTTGATTCAGGAAATCAAGCTGAGTTTCTCCGCTTGAGTGAATGATTC 250
332 roGluGlyGlyProGlyGlyAsnIleLeuGlyGlnLeuAlaAlaVal 348
|||||
251 CTGAGGCTGCTCTCGAGGGAACATCTAGTCACTGCGACCTGCTGTG 300
349 ProGlnThrLeuThrValThrProGluGluArgGluAlaIleGlnArg 365
|||||
301 CCACAAACGCTGACACTTACCCAGAGGAGGAGGAGGACTATCCAGCGCT 350
365 ucLuglMetGlyPheAsnArgGluLeuValLeuGlnValAlaPheAla 382
|||||
351 CAGGGAATGGGGTTCAACCGTGAGCTTGCTAGAAAGTTTCTTTGCAT 400
382 yaAsnLysAspGluGluLeuThrAlaAsnTyrLeuLeuAspHisGlyHis 398
|||||
401 GCAACAAGACGAAAGAGCTTACAGCCCACTACCTTGTGATCATGGCAT 450
399 GluPheAspAspGlnGln 405
|||||
451 GAGTTTGACGACGACGACCA 471

seq_name: gb_est2:BG445328

seq_documentation_block:
LOCUS BG445328 810 bp mRNA linear EST 15-MAR-2001
DEFINITION GA_Ea0027L22f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0027L22f, mRNA sequence.
ACCESSION BG445328
VERSION BG445328.1 GI:1354980
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE
1 (bases 1 to 810)
AUTHORS Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
'D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGCG
High quality sequence stop: 767.
FEATURES
location/Qualifiers
source 1..810
/organism="Gossypium arboreum"
/strain="AKA"
/db_xref="taxon:29729"
/clone_id="GA_Ea0027L22f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/note="Vector: pBR-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 212 a 204 c 198 g 193 t
ORIGIN
align_scores:

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Quality: 781.50 Length: 269
 Ratio: 3.618 Gaps: 8
 Percent Similarity: 80.297 Percent Identity: 63.197

alignment block:
 US-09-805-550-2 x BG445328 ..

Align seg 1/1 to: BG445328 from: 1 to: 810

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82 SerGlyAlaSerThrAlaThrAlaValAlaProAlaThrLeuAlaI 98
   ||| ||||| ||||| ||| ||||| |||
7 TCACAGCTTCAACAGCTCTCTACAAAGAAAGCTCTGAGGACGTAATCT 56
   ||||| ||||| ||||| ||||| |||||
98 nProAlaAlaProValAlaProAlaAlaSerValAlaArgThpProThrg 115
   ||||| ||||| ||||| ||||| |||||
57 GCACACAGCTGCCA...GCACACAGCTCTACT..... 84
   ||||| ||||| ||||| ||||| |||||
115 lnaAlaProValAlaThrAlaIuThrAlaProProSerValAlaProGln 131
   ||||| ||||| ||||| ||||| |||||
85 ..GCACCTGTCACAGCTCAGTATGCT....GCAGTGCCTACTGAA 126
   ||||| ||||| ||||| ||||| |||||
132 AlaAlaProAlaAlaThrValAlaAlaAlaThrAspAlaAlaPylTyrSe 148
   ||||| ||||| ||||| ||||| |||||
127 TCAGCTCTGCTGCTCTCAAGTACTCTTGTGAGATCTGATGTTATG 176
   ||||| ||||| ||||| ||||| |||||
148 rGlnAlaAlaSerAsnLeuValAlaPheGlyAsnAsnLeuGlnThrIleg 165
   ||||| ||||| ||||| ||||| |||||
177 CCAGAGCAGCATCTACCTGCTGTCAGGAGTAATCTAGAGCAACATCC 226
   ||||| ||||| ||||| ||||| |||||
165 lnlGlnIleuAspMetGlyGlyGlyThpTrpGluArgAspThrValAla 181
   ||||| ||||| ||||| ||||| |||||
227 AACAGATCTCTTGATATGGGTGAGGACCTGGGACAGGACACTGTGTC 276
   ||||| ||||| ||||| ||||| |||||
182 ArgAlaLeuArgAlaAlaTyrAsnAsnProGluArgAlaIleAspTyrle 198
   ||||| ||||| ||||| ||||| |||||
277 CAGGCCCTTGCTGCTGCTTATATTAACCCAGAGAGCTGTGATATTT 326
   ||||| ||||| ||||| ||||| |||||
198 uTyrSerGlyIleProGluAsnValGluAlaGlnProValAlaArgAlaP 215
   ||||| ||||| ||||| ||||| |||||
327 GATATTCGGCATCCCGAGCAGCATGMAAGCTCCACCTGTCGCCGTGCTC 376
   ||||| ||||| ||||| ||||| |||||
215 rAlaAlaIaGlyGlnGlnThrAsnGlnGlnIleAlaSerProAlaGlnPro 231
   ||||| ||||| ||||| ||||| |||||
377 CTGTAGTGGGCAACACCAAC...TCTGCTGACAACTCAACAGCT 423
   ||||| ||||| ||||| ||||| |||||
232 AlaValAlaLeuProValGlnProSerProAlaSerAlaGlyProAsnAl 248
   ||||| ||||| ||||| ||||| |||||
424 GCACAAACGGCAGCTATT.....CTGCAAGT...GGACCAATGC 461
   ||||| ||||| ||||| ||||| |||||
248 aAsnProLeuAsnLeuPheProGlnGlyValProSerGlyGlySerAsn 265
   ||||| ||||| ||||| ||||| |||||
462 AATTCATTCAGACCTCTTCCAGGCGCTCCCAACATCGGTGCAAGT. 510
   ||||| ||||| ||||| ||||| |||||
265 rGlyValValProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGln 281
   ||||| ||||| ||||| ||||| |||||
511 .....GGTGTGGGGGTGGCACTCTGTGATTTTTCAGGAAC 546
   ||||| ||||| ||||| ||||| |||||
282 LeuProGlnPheGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGlnI 298
   ||||| ||||| ||||| ||||| |||||
547 AGTCACACAGTTTCAAGCTTGGCGAAGATGTGCAAGCCAAATCCACAAT 596
   ||||| ||||| ||||| ||||| |||||
298 eLeuGlnProMetLeuGlnGlnLeuGlyLysGlnAsnProGlnIleLeu 315
   ||||| ||||| ||||| ||||| |||||
597 AATGCAAGCCATGCTTCACAGAGTTGGGAAACAAATCCAAATTAATGA 646
   ||||| ||||| ||||| ||||| |||||
315 rGlyLeuIleGlnIuAsnGlnAlaGlnPheLeuArgLeuValaAsnGln 331
   ||||| ||||| ||||| ||||| |||||
647 GACTTATTCACAGACATCAGGAGTACCTTCTGCTGATCAATGAAGACT 696
   ||||| ||||| ||||| ||||| |||||
332 ProGlnGlyLysProGlyAsnIleLeuGlyGlnIleuAlaAlaAla 348
   ||||| ||||| ||||| ||||| |||||
697 GCGAAGAGGTGAGAG...GGAACATTTNTGGGCAATTACTCTAGAGCAT 743
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348 lProGln 350
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 744 GCCACAG 750

seq_name: gp_est2:BG365760

seq_documentation_block:

LOCUS BG365760 906 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSM10004B16f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
 (20 DAP) Hordeum vulgare cDNA clone HVSM10004B16f, mRNA sequence.
 ACCESSION BG365760
 VERSION BG365760.2 GI:16323859
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 906)
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
 , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Chol, D.W., Fenton
 , R.D., Close, S.J., Oates, R. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex 20 DAP spike cDNA library
 Unpublished (2001)
 On Mar 8, 2001 this sequence version replaced gi:13254859.
 CONTACT: Wing RA
 CLEMSON UNIVERSITY
 CLEMSON UNIVERSITY GENOMICS INSTITUTE
 100 JORDAN HALL, CLEMSON, SC 29634, USA
 TEL: 864 656 7288
 FAX: 864 656 4293
 EMAIL: twing@clermson.edu
 Total bp bases = 406
 Seq primer: AATTAACTCCTCACTAAAGCG
 High quality sequence stop: 657.
 Location/Qualifiers

FEATURES

source

/organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSM10004B16f"
 /clone_lib="Hordeum vulgare 20 DAP spike EST library
 HVCDNA0010 (20 DAP)"
 /issue_type="20 DAP spike"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP. Site_1: BcoRI. Site_2: XhoI;
 Plants were grown in the greenhouse at the University of
 California, Riverside (Fenton, SJ Close, TJ Close). Whole
 spikes with awns trimmed were collected at 20 DAP (Fenton
). Total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, and 1 million
 pfu were in vivo excised to give phagescript SK(-) cDNA
 phagmids in the TJ Close lab at the University of
 California, Riverside (Choi). Phagmids were plated and
 picked at the Clemson University Genomics Institute (CUGI)
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 , Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/gsgpages/bgn/31/cover.html)"
 BASE COUNT 206 a 246 g 212 t 1 others
 ORIGIN

alignment_scores:
 Quality: 781.50 Length: 287
 Ratio: 3.383 Gaps: 10
 Percent Similarity: 80.488 Percent Identity: 65.505

alignment_block:
 US-09-805-550-2 x BG365760 ..

Align seg 1/1 to: BG365760 from: 1 to: 906

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1 MetLysLeuAsnValIleuThrLeuLysGlyThrAsnProGluIleGluAl 17
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67 ATGAAGCTCAACGTAAAGACCTCAAGGACACACCTTCGAGATGAGGCG 116
  |||||||
17 ASerProAspAlaSerValAlaAspValLysArgIleIleGluThrThrG 34
  |||||||
117 GACCCCGAGTCCGCGTGGGTGAGCAAGAGACTCATCGAGAGTGCCTC 166
  |||||||
34 InglyGlnSerThrTyrArgAlaAspGlnGlnMetLeuIleTyrGlnGly 50
  |||||||
167 AGGGGCAAAATGTGACCCCTCGCATCAGCTGATCATATATCAAGCA 216
  |||||||
51 LysIleLeuLysAspGluThrThrLeuGlnSerAsnGlyValAlaGluAs 67
  |||||||
217 AAAATCTGAAAGATGATACCACTCTGATGCTATCAAGGTTGCGAGAGA 266
  |||||||
67 nSerPheLeuValIleMetLeuSerLysAlaLysAlaSerSerSerGlyA 84
  |||||||
267 CAGTTCCTGTTATATGCTGTCTAAGCCATGAGCGTCATCTAGTGGCG 316
  |||||||
84 lAserThrAlaThrThrAlaLysAlaProAlaThrLeuAlaGlnProAla 100
  |||||||
317 CTCTTCCTGCT....TCAAAGCACCTGTTAGTCAGTCTCAACCTGCT 360
  |||||||
101 AlaProValAla.....ProAlaAlaSerValAlaAla 111
  |||||||
361 ACCCAGAGTGTGCTGCTACTACCTGCTGCTGCTGCTGCTGCTGCTGCA 410
  |||||||
111 gThr...ProThrGlnAlaProValAlaThrAlaGlnThrAlaProPro 127
  |||||||
411 ATCAACACCTTCGCAAGCACCTGTTGTCATGATCAACCGGCTCCCA 460
  |||||||
127 eValGlnProGlnAla.....AlaProAlaAlaThrAlaAlaAla 140
  |||||||
461 GTGCACACACTTCACGCTGTTCTGATCTCCAGCTGCTGCACTAAGTGA 510
  |||||||
141 ThrAspAspAlaAspValTyrSerGlnAlaAlaSerAsnLeuValIle 157
  |||||||
511 TCAGCGCATGCTGATGATACAGTCAAGCTGATCAAACTTCTCTCGG 560
  |||||||
157 yAsnAsnLeuGlnGlnThrIleGlnGlnIleLeuAspMetGlyGlyT 174
  |||||||
561 CGGCATCTAGAACAGACAGTCCATCAATCTTGACATGGGTGGTGCA 610
  |||||||
174 hTrPgluArgAspThrValValArgAlaLeuArgAlaAlaLeuTrpAsn 190
  |||||||
611 CCGTGAAGCTTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
  |||||||
191 ProGluArgAlaIleAspTyrLeuTyrSerGlyIleProGluAspValG 207
  |||||||
661 CCGTAGAGGCGTATGACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
  |||||||
207 uAlaGlnProValAlaArgAlaProAlaAlaGly..GlnGlnThrAsnG 223
  |||||||
711 GGCCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
  |||||||
223 nGlnAlaAlaSerProAlaGlnProAlaValAlaLeu..ProValAla 239
  |||||||
761 TCAGGCTCAATTCATGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 810
  |||||||
240 Ser...ProAlaSerAlaGlyPro..AsnAlaAsnProLeuAsnLeuP 255
  |||||||
811 TCTGTGGGGGTCTCTGTGGGGCTTAAGCAAAATCTTAAACCTTTT 860
  |||||||

```

255 roGlnGlyVal.ProSerGlyLysSerAsnProGlyValProGlyAl 271
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 861 CACAGGCTGTGCGGTGGGTGGGGCC.....ATTCCTGGGCC 898

271 agly 272
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 899 CGGA 902

seq_name: gb_estl:AV928200

seq_documentation_block:

LOCUS AV928200 750 bp mRNA linear EST 18-JAN-2002
 DEFINITION AV928200 K. Sato unpublished cDNA library, cv. Haruna Nijo second
 leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA
 clone basd27f18 3', mRNA sequence.

ACCESSION AV928200
 VERSION AV928200.1 GI:18223997

KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare.
 ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE 1 (bases 1 to 750)
 Sato, K., Saitoh, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 Unpublished (2002)
 CONTACT: Tadasu Shin-1
 CENTER FOR GENETIC RESOURCE INFORMATION
 NATIONAL INSTITUTE OF GENETICS
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

FEATURES
 source location/Qualifiers
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 /organism="Hordeum vulgare subsp. vulgare"
 /cultivar="Haruna Nijo"
 /db_xref="taxon:112509"
 /clone="basd27f18"
 /clone_1lb="K. Sato unpublished cDNA library, cv. Haruna
 Nijo second leaf stage seedling leaves"
 /issue_type="seedling leaves"
 /dev_stage="second leaf stage"
 BASE COUNT 190 a 194 c 181 g 183 t 2 others
 ORIGIN

alignment_scores:
 Quality: 774.00 Length: 194
 Ratio: 4.423 Gaps: 2
 Percent Similarity: 90.206 Percent Identity: 81.443

alignment_block:
 US-09-805-550-2 x AV928200/rev ..

Align seg 1/1 to reverse of: AV928200 from: 1 to: 750

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213 ArgAlaProAlaAlaGlyGlnGlnThr...AsnGlnAlaAlaSerPr 228
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750 CGAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 701
  |||||||
228 oAlaGlnProAlaValAlaLeuProValGlnProSer...ProAlaSer 244
  |||||||
700 GGCTCAGCTGCACTCTACCGCGAGTGCAGCATCTGTGCTGCTGCTG 651
  |||||||
244 lAglyProAsnAlaAsnProLeuAsnLeuPheProGlnGlyValProSer 260
  |||||||
650 CTGGGCTCAATGCGAATCCTTAACCTTTCCACAGGCTGCTCCAGT 601
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261 GlyGlySerAsnProGlyValValProGlyAlaGlySerGlyAlaLeuAs 277
  |||||||

```

```

600 GGTGGGGCCAATGCTGCTGCTGGTGGTGCCGCGTCCCGTCCCTTGA 551
277 PALaleuArgGlnLeuProGlnPheGlnAlaLeuLeuGlnLeuValGlnA 294
|||||
550 TGCATTGCGACAGCTTCCACAGCATGCTCTTGCATTGGTCCAGG 501
|||||
294 IAsnProGlnIleLeuGlnProMetLeuGlnIleuGlyLysGlnAsn 310
|||||
500 CPAATCCCAAAATCTTACAGCCCAATGCTTCAAGAGCTGGGGAAACAAT 451
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311 ProGlnIleLeuArgLeuIleGlnGluAsnGlnAlaGluPheLeuArgLe 327
|||||
450 CCAAGATCCTGCGGTGATTCAGGAAATCAGGCTGAGTTCTCCGCT 401
|||||
327 uValAsnGluSerProGlnGlyGlyProGlnGlyAsnIleLeuGlyGlnL 344
|||||
400 GGTAAATGAACAACCTGAGAGTGCTGGCGGAATATACTAGCGCAC 351
|||||
344 euAlaIaIaValProGlnThrLeuThrValThrProGlnGluArgGlu 360
|||||
350 TGGCAGCTCAAAATGCCACAGGCAAGTTCAGTTACTCCAGAAACGGGAG 301
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361 AlaIleGlnArgLeuGlnGlyMetGlyPheAsnArgGluLeuValLeuG 377
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300 GCCATCCAGCGGCTTGAGTCAATGGGTTCAATGCTGAGCTTGTTGA 251
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377 uValPhePheAlaCysAsnLysAspGlnGluLeuThrAlaAsnTyrLeuL 394
|||||
250 GGTCTTCTTGCATGCAACAGGATGAAGAACTGGTCCCAACTATCTTT 201
|||||
394 euAspHisGlyHisGluPheAspAspGlnGln 404
|||||
200 TGGATCATGGCCACGAGCTTGAGGACACACAA 169

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